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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                        Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Run
                                                                                                                                                                                                                                        Database
                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OM protein - protein search, using sw model
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     10:
11:
12:
13:
14:
                                                                                                                                                                                                                                        SPTREMBL_15:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-331-631A-8_COPY_33_79
275
                                                                                                                                                                                                                                                                                                                                                                                                                         374700 seqs, 117207915 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               March 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GDDDPPKRYEDCRRCEWDT.....QCEESCKSQYGEKDQQQRHR 47
                                                                                     sp_phage: *
                                                                                                                                    sp_mammal:*
                                                                                                                                                                    sp_human:*
                                                                                                                                                                                     sp_fungi:*
                                                                                                                                                                                                                   sp_archea:*
                                                                                                     sp_organelle:*
                                                                                                                     sp_mhc:*
                                                                                                                                                      sp_invertebrate:*
                                                                                                                                                                                                       sp_bacteria:*
                               sp_rodent:*
sp_virus:*
sp_unclassified:*
                   sp_vertebrate:*
                                                                sp_plant:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2001, 16:09:31; search time 299.73 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (without alignments)
18.379 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

19	18	17	16	15	14	13	12	11	10	9	8	7	σ	ر ت	4	u	2		Result No.
60.5	60.5	61	61.5	62	62.5	63.5	63.5	64	65	65.5	67.5	82.5	88	90	92	94	105.5	124	Score
22.0	22.0	22.2	22.4	22.5	22.7	23.1	23.1	23.3	23.6	23.8	24.5	30.0	32.0	32.7	33.5	34.2	38.4	45.1	Query Match 1
238	160	204	238	525	103	246	242	1298	554	411	541	393	625	810	666	666	593	525	Query Match Length DB
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081257	Q9SQH1	016405	081255	Q9VSC2	Q9J1K0	081261	081260	Q9P2D9	Q9VPS3	P91419	Q9V7P3	Q9ZTPO	Q9SPL3	Q9ZWI3	Q9SPL5	Q9SPL4	Q9SEW4	Q43358	ID
081257 zea luxuria	Q9sqhl arachis hyp	016405 caenorhabdi	081255 zea mays su	Q9vsc2 drosophila	Q9jik0 rattus norv	O81261 tripsacum d	081260 tripsacum d	Q9p2d9 homo sapien	Q9vps3 drosophila	P91419 caenorhabdi	Q9v7p3 drosophila	Q9ztpO oryza sativ	Q9spl3 macadamia i	Q9zwi3 cucurbita m	Oi	_	Q9sew4 juglans reg	Q43358 theobroma c	Description

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20
9.	9.	9.	9.	9.	9	59.5	9.	9	9	9	9	9	9	60	60	60	60	60	60	60			•	60.5	
•	•		•	•	•	21.6	•	•	•	•	•	21.6	•	•	21.8	٠		21.8						•	22.0
240.	240	239	238	238	238	238	238	236	236	230	191	163	122	1927	835	811	774	774	456	241	3469	1819	1327	897	396
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081256	081252	Q9SBF1	Q9S6Z6	Q9SBE5	Q9SBE8	081258	081249	Q9SBF2	081250	Q9X1D9	Q9N0L8	090098	Q03863	025262	Q9V744	Q926K5	Q9JSK8	Q9K1Z4	Q9Z9G3	Q9K1Y2	Q9U4I2	Q9ZLV0	Q9NFB4	Q17336	Q9NSJ1
zea mays		zea ı	zea	zea luxur	Q9sbe8 zea mays su	58 zea luxur	zea mays	zea mays	0	thermotoc		ιpanze	w		drosophila	chlamydia	Q9jsk8 chlamydia p		chlamydia	2 chlamydia	_	Q9zlv0 helicobacte	Q9nfb4 plasmodium	Q17336 caenorhabdi	Q9nsj1 homo sapien

ALIGNMENTS

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RESULT PAGE BEFORE SOLUTION AND PAGE SOLUTION AN
       В
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                                                                                                                                 Query Match
Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                        Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                         CHAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=92283309; PubMed=1600151;

WCHENTY L., Fritz P.J.;

"Comparison of the structure and nucleotide sequences of vicilin genes of cocoa and cotton raise questions about vicilin evolution.";

Plant Mol. Biol. 18:1173-1176(1992).

EMBL; X6265; CAAA44493.1; -.

EMBL; X62626; CAAA4494.1; -.

EMBL; X62637; PHL.

MENDEL; 30919; Thecc;1188;30919.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CSV.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
TISSUE=LEAVES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Theobroma cacao (Cacao).

Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Budicotyledons; core eudicots; Rosidae; eurosids II; Malvales; Malvaceae; Theobroma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VICILIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INTERPRO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=3641;
       37
                                      4 DPPKRYEDCRRRCEWDTRGQKEQQQCEESCKSQYGEKDQQQ 44
DPRQQYEQCQRRCESEATEEREQEQCEQRCEREYKEQQRQQ 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPR001113; -
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25
525 AA;
                                                                                                                                 Conservative
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                                                                                                                                                                    45.1%;
46.3%;
                                                                                                                                                                                                                                                                                           24 POTENTIAL.
525 VICILIN.
60798 MW; 19114CD5C248905D CRC64;
                                                                                                                                 12;
                                                                                                                                                                    Score 124; DB 10;
Pred. No. 5.2e-08;
                                                                                                                                 Mismatches
                                                                                                                                 10;
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Best Local S
Matches 18
   Query Match
Best Local :
                                                                                                                                                                                                                                                                                         A ramily of antimicrobial peptides is produced globulin proteein in Macadamia integrifolia."; plant J. 0:0-0(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9SPL4; PRELIMINARY; Q9SPL4; 13; Q1-MAY-2000 (TrEMBLrel. 13; Q1-MAY-2000 (TrEMBLrel. 15; Q1-OCT-2000 (TrEMBLrel. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OSSEW4;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
VICILIN-LIKE PROTEIN PRECURSOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Juglans regia (English walnut).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
Fagales; Juglandaceae; Juglans.
NCBI_TaxID=51240;
                                                                                                                                              PFAM; PF00546;
SEQUENCE 666
                                                                                                                                                                                                                                             EMBL; AF161884; AAD54245.1; HSSP; P02853; 2PHL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Macadamia integrifolia (Macadamia nut).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
Magnoliophyta; eudicotyledons; Proteaceae; Macadamia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AMP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VICILIN PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PFAM; PF00546; Seedstore_7s; NON_TER 1 1 1 SEQUENCE 593 AA; 69990 MW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases EMBL; AF066055; AAF18269.1; -. HSSP; P02853; 2PHL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=CV. SUNLAND; TISSUE=SOMATIC EMBRYO LINE; Teuber S.S., Jarvis K.C., Peterson W.R., Dandekar A.M., Ansari A.A.; "Identification and cloning of a cDNA encoding a vicilin-like protei Jug r 2, from English walnut kernel (Juglans regia): a major food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                    INTERPRO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=NUT KERNEL;
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les 18; Conserv
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   Similarity
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IPR001113; -
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                                                                                                                                              Seedstore_7s;
AA; 78243 MW;
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Best Local Similarity 33.3
Matches 15; Conservative
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01-MAY-1999
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Q9SPL5;
01-MAY-2000
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Marcus J.P., Goulter K.C., Green J.L.,
Marcus J.P., Goulter K.C., Green J.L.,
"A family of antimicrobial peptides is
"A family of antimicrobial peptides is
                                                                                                                                      Yamada K., Shimada T., Kondo M., Nishimura 'Multiple functional proteins are produced of a single precursor by vacuolar processin J. Biol. Chem. 274:2563-2570(1999).
                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-KUROKAWA AMAKURI NANKIN;
                                                                                                                                                                                                                                                                                                                                         Cucurbita maxima (Pumpkin) (Winter sque 
Eukaryota; Viridiplantae; Embryophyta; 
Magnoliophyta; eudicoryledons; core eu 
Cucurbitales; Cucurbitaceae; Cucurbita
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                globulin protein in Macadam
Plant J. 0:0-0(1999).
EMBL; AF161883; AAD54244.1;
HSSP; P02853; 2PHL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
INTERPRO; IPRO01113; -.
PFAM, PF00546; Seedstore_7s;
PRODOM; PD081059; -; 1.
SEQUENCE 810 AA; 97314 MW;
                                                                                       EMBL; AB019195; BAA34056.1; HSSP; P02853; 2PHL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Macadamia integrifolia (Macadamia nut).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
Magnoliophyta; eudicotyledons; Proteaceae; Macadamia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AMP2
                                                                                                                                                                                                                               MEDLINE=99107919; PubMed=9891029;
                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=3661;
                                                                                                                                                                                                                                                                                                                                                                                                                                     PV100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INTERPRO; IPR001113; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PF00546; Seedstore_7s;
VCE 666 AA; 78217 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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Last annotation updat
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ptides is produced by p
integrifolia kernels."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C752B884B2DF0224 CRC64;
    A829A3F7542266AB
                                                                                                                                                                                                                                                    TISSUE=COTYLEDON;
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annotation updat
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                                                                                                                                                           M., Hara-Nishimura
by cleaving Asn-Glr
ng enzyme.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 666;
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Query Match

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Marcus J.P., Goulter K.C., Greer
"A family of antimicrobial pepti
globulin protein in Macadamia ir
Plant J. 0:0-0(1999).
EMBL; AF161885; AAD54246.1; -.
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01-MAY-1999
01-MAY-1999
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Eukaryota; Viridiplantae; Embryophyta; Trac
Maanollophyta; eudicotyledons; Proteaceae;
                                                                                                                                                                                             Chen P.W., Chen L.J.; Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases EMBL; AF049348; AAD02494.1; -.
                                                                                                                                                                                                                                                                                                                                                                      Oryza sativa (Rice).
Eukaryota; Viridiplantae;
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01-MAY-1999 (TrEMBLrel.
HYPOTHETICAL 45.3 KDA PI
                                                                                                                                                  Hypothetical protein. SEQUENCE 393 AA; 4
                                                                                                                                                                                                                                                                                                                             Magnoliophyta; L
NCBI_TaxID=4530;
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                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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GDDDPPKRYEDCRRRCEWDT-RGQKEQQQCEESC--KSQYGEKDQQQRH
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                                                                  Similarity
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                                                                                                                                                      45258 MW;
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29.5%;
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13, Last sequence up
15, Last annotation
                                                                                                                                                                                                                                                                                                                                                                        Embryophyta; Tracheophyta; Spermatophyta;
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                                           13;
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Last annotation update)
                                    Score 82.5; DI
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13; Mismatches
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                                                                                                                                                                                                                                                                                                                                                    Poaceae; Oryza
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RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Brandon R.C., Rogers Y. H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Baster E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Byraktaroglu L., Beasley E.M.,
RA Besson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Ghris K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
RA Ghris K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
RA Ghris J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Durbin K.J., Evangelista C.C., Ferracz C., Ferriera S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegvam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA McIntosh T.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Harris N.L., Remington K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Cherry S., Senth R., Saunders R.D.C., Scheeler F., Shen H.,
RA Shime B.C., Siden-Kiamos I., Simbson M., Skubski M.P., Smith T.,
                                                                                                                                                         Query Match
Best Local
                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                      Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang Z. Y., Wassarman D.A., Weinstock G.M., Weissenbach J. Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Ya Ye J., Yeh R. F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster."; Science 287,2185-2195(2000).
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01-MAY-2000
01-MAY-2000
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Q9V7P3;
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Pterygota; Neoptera;
                                                                                                                                                                                                                                                                                                               FLYBASE;
                                                                                                                                                                                                                                                                                                                                                   EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Adams M.
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      234
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                                                          DDDPPKRYEDCRRRCEWDTR--GQKEQQQCEESCKSQYGEKDQQQRHR
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SE; FBgn0034121; CG6262
                                                                                                                               19;
                                                                                                                                                         Similarity
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O (TrEMBLrel. 13,
O (TrEMBLrel. 13,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        melanogaster (Fruit fly).
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                                                                                                                           Conservative
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-DC--ECSMDERQKQQMEQQQKQQDCMRQ--QQQQQQEHQ
                                                                                                                                                                                                                                                                                     58080
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39
                                                                                                                                                         . 5%;
                                                                                                                                                                                                                                                                                     W.
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Last sequence up
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Pred.
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                                                                                                                                                                                                                                                                                  83BEA5FE510F7C8F CRC64;
                                                                                                                           Mismatches
                                                                                                                                                         67.5;
No. 0.
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8
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                                                                                                                                                                                   Length 541;
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, Baldwin D.,
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                                                                                                                        11;
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RESULT QPYPS3
IDVPS3
IDVPS3
IDVPS9
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DT 011
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DT 011
RF CGG
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P91419
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Best Local S
Matches 14
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Q9VPS3;
01-MAY-2000 (
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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.,
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
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                      STRAIN-BERKELEY;
MEDLINE-20196006;
                                                                                                                                                                       Eukaryota; Metazoa; Arthropoda; Tracheata; Pterygota; Neoptera; Endopterygota; Diptera
                                                                                                                                                                                                                          Drosophila melanogaster (Fruit fly)
                                                                                                                                                                                                                                                      CG2839
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                                                                            SEQUENCE FROM N.A.
                                                                                                                                                      Ephydroidea;
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Bradshaw H., Wohldmann
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MEDLINE=94150718; PubMed=7906398;
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                                                                                                                          NCBI_TaxID=7227;
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  M.D.,
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  06006; PubMed=10731132; Celniker S.E., Holt R.A.,
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                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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                                                                                                                                              eoptera; Endopterygota; Diptera;
Drosophilidae; Drosophila.
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08, Last annotation update)
CDNA YK115A6.5.
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Pred. No. 1.1;
11; Mismatches
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  Evans
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                                                                                                                                                                                              Hexapoda;
C.A.,
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                                                                                                                                                                     Brachycera;
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  Gocayne
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                                                                                                                                                                       Muscomorpha;
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J.D.,
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RA George R.A., Lewis S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Mixlos G.L.G.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Mixlos G.L.G.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Mixlos G.L.G.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Mixlos G.L.G.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Mixlos G.L.G.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Mixlos G.L.G.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktargulu L., Beesley E.M.,
RA Beeson K.Y. Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Berson K.Y. Benos P.N., Bounck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Ghoritis K.C., Busam D.A., Butler H., Gadieu E., Certer A., Chandra I.,
RA Ghoden K., Doup L.E., Downes M., Dugan Rocha S., Dubkov B.C., Dun P.,
RA Goder K., Bouch S., Downes M., Dugan Rocha S., Dubkov B.C., Dun P.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hilliam J., Waltel B., McIntosh T.C., Krettiz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Krettiz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Krettiz S., Kulp D., Lai Z.,
RA McIntosh T., Levitsky A.A., Li J., Li Z., Llang Y., Lin X.,
Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.L.,
RA McIntosh T.S., Nanders R.D.C., Scheeler F., Shen H.,
RA McIntosh T.S., Pollard J., Puri V., Reese M.G.,
RA Mang Z.-Y., Massarman D.A., Weinster B.D.C., Scheeler F., Shen H.,
RA Harris M., Walley H., Marphy B., Murphy L., Munny D., Yang A.H., Wang X.,
Ra H
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                Q9P2D9 PRELIMINARY;
Q9P2D9;
01-OCT-2000 (TremBLrel. 15,
01-OCT-2000 (TremBLrel. 15,
01-OCT-2000 (TremBLrel. 15,
                      TISSUE=BRAIN;
Nagase T., Kikuno R.,
                                                             SEQUENCE FROM N.A
                                                                                                                      Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                             Homo sapiens (Human)
                                                                                                                                                                                   KIAA1408
                                                                                                                                                                                                    KIAA1408
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Prediction of the coding sequences of unidentified human genes.XVI.
                                                                                                                                                                                                                                                                                                                                                                                                 468 RRREEKRRREEEERRKEEEERRKEEERRKDEERR 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NTERPRO;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      7 KRYEDCRRRCEWDTRGQKEQQQCEESCKSQYGEKDQQQR 45
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TE; PS50041; C_TYPE_LECTIN_2; 1.
ER 554 554
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                      Ishikawa K., Hirosawa
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                                                                                                                                                                                                                    Last annotation update)
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                                                                                                                                                                                                                                        Last sequence update)
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                                                                                                                      Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                    PRT;
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Matches 15
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Best Local
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SEQUENCE FROM N.A.
Hilton H., Gaut B.S.;
Hispeciation and domestication in
"Speciation and domestication in
evidence from the Globulin-1 gen
Genetics 0:0-0(1998).
EMBL: APG064235; AAC31478.1; -.
HSSP; P50477; ICAU.
                                                                                                                                                                                                                                                              Ol-OCT-2000 (1988)
GLOBULIN-1 (FRAGMENT).
Tripsacum dactyloides (Gama grass).
Tripsacum dactyloides (Embryophyta;
Eukaryota; Viridiplantae; Embryophyta;
Poaces; Poaces; Poaces; Poaces; Poaces; Poaces;
                                                                                                                                                                                                                                                                                                                                                                                     O81261;
01-NOV-1998 (TrEMBLrel. 08,
01-NOV-1998 (TrEMBLrel. 08,
01-OCT-2000 (TrEMBLrel. 15,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tripsacum dactyloides (Gama grass).
Eukaryota; Viridiplantae; Embryophyta; Traci
Magnoliophyta; Liliopsida; Poales; Poaceae;
NCBL_TaxID=4563;
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01-NOV-1998 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
GLOBULIN-1 (FRAGMENT).
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01-NOV-1998
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                                                                                                                                                                                                                                           Magnoliophyta; Liliopsida;
NCBI_TaxID=4563;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [NTERPRO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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nes 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ω
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DDPPKRYEDCRRRCEWDTRGQKEQQQCEESCKSQYGEKDQQQRHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AF064234; AAC31477.1; -. P50477; 1CAU.
L; 31902; Trida;1188;31902.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    H., Gaut B.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              l Similarity
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ceae; Tripsacum
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RESULT
Q9VSC2
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Q9JIK0
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Best Local
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Best Local
                                                                                   Drosophila melanogaste
Eukaryota; Metazoa; Ar
Pterygota; Neoptera; E
Ephydroidea; Drosophil
                                                                                                                                                                                                                                                                                                                                                    NON_TER
SEQUENCE
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01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-QCT-2000 (TrEMBLrel. 15,
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         MEDLINE=20196006; PubMed=10731132; Adams M.D., Celniker S.E., Holt R.A., E. Amanatides P.G., Scherer S.E., Li P.W.,
                                           SEQUENCE FROM N. STRAIN-BERKELEY;
                                                                          Ephydroidea; Drosophilidae;
NCBI_TaxID=7227;
                                                                                                                                CG8254
                                                                                                                                          CG8254 PROTEIN.
                                                                                                                                                                                                 Q9VSC2
                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                              J. Neurosci.
                                                                                                                                                                                                                                                                                                                                                                                                         Specific. "
                                                                                                                                                                                                                                                                                                                                                                                                                    Channel
                                                                                                                                                                                                                                                                                                                                                                                                                                       Pan J.Q., Lipscombe
                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-SPRAGUE-DAWLEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VOLTAGE GATED N-TYPE CALCIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00867; CPSASE_2; UNKNOWN_1.
NON_TER 246 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PFAM; PF00546; Seedstore_7s; 1
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                                                                                                                                                                                                                                                       55
                                                                                                                                                                                                                                                                                                Local Similarity
mes 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38 CARRCE--DRPWHQRPRCLEQCREEEREK-QQERSR 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12 CRRRCEWDTRGQKEQQQCEESCKSQYGEKDQQQRHR 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
les 15; Conserv
                                                                                                                                                                                                                                                                 6 PKRYEDCRRRCEWDTR-GQKEQQQCEESCKSQYGEKDQQQRHR
                                                                                                                                                                                                                                                     PRQQNSAKARSVWEQRASQLRLQNLRASCEALYSEMDPEERLR
                                                                                                                                                                                                                                                                                                                                                                                    AF222337;
                                                                                             melanogaster (Fruit fly).
Metazoa; Arthropoda; Tracheata; He
Neoptera; Endopterygota; Diptera;
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103 7
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Last annotation update)
M CHANNEL ALPHAIB (FRAGMENT).
                                                                                     Drosophila
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Pred. No. 0.72;
8; Mismatches 21;
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          Evans C.A.
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s C.A., wins R.A.,
                                                                                                         Hexapoda; Insecta;
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                                                                                              Brachycera;
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                                                                                                                                                                                                                                                                       Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PRO0024; HOMEOBOX.

PROSITE; PS00027; HOMEOBOX_2; 1.

PROSITE; PS50071; HOMEOBOX_2; 1.

SEQUENCE 525 AA; 56769 MW; 2F361B164D982EFE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INTERPRO; IPR001356; -. PFAM; PF00046; homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FLYBASE; FBgn0035828; CG8254.
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                                                                                                                                   467 PKRFEVASGLMLSETQVKIWFQNRRMKW-KRSKKAQQEAKERAKANQQQQQQQQ 519
                                                                                                                                                                                   6 PKRYEDC------RRRCEWDTRGQKEQQQCEESCKSQYGEKDQQQ 44
                                                                                                                                                                                                                                              1 Similarity
16; Conserv
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                         1, 2001, 16:09:33
                                                                                                                                                                                                                                                                  22.5%;
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